

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Choi et. al.

(ii) TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

(iii) NUMBER OF SEQUENCES: 452

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.
(B) STREET: 9410 Key West Avenue
(C) CITY: Rockville
(D) STATE: Maryland
(E) COUNTRY: USA
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
(B) COMPUTER: HP Vectra 486/33
(C) OPERATING SYSTEM: MSDOS version 6.2
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Unassigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/961,083
(B) FILING DATE: OCT-30-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Michelle S. Marks
(B) REGISTRATION NUMBER: 41,971
(C) REFERENCE/DOCKET NUMBER: PB340P2C1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504
(B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TAAAATCTAC GACAATAAAA ATCAACTCAT TGCTGACTTG GGTTCTGAAC GCCCGTCAA	60
TGCCCAAGCT AATGATATTG CCACAGATTT GGTTAAGGCA ATCGTTCTA TCGAAGACCA	120
TCGCTTCTTC GACCACAGGG GGATTGATAC CATCCGTATC CTGGGAGCTT TCTTGCGCAA	180
TCTGCAAAGC AATTCCCTCC AAGGTGGATC AACTCTCACC CAACAGTTGA TTAAGTTGAC	240
TTACTTTCA ACTTCGACTT CCGACCAGAC TATTTCTCGT AAGGCTCAGG AAGCTTGGTT	300
AGCGATTCAAG TTAGAACAAA AAGCAACCAA GCAAGAAATC TTGACCTACT ATATAAATAA	360
GGTCTACATG TCTAATGGGA ACTATGGAAT GCAGACAGCA GCTCAAAACT ACTATGGTAA	420
AGACCTCAAT AATTAAAGTT TACCTCAGTT AGCCTTGCTG GCTGGAATGC CTCAGGCACC	480
AAACCAATAT GACCCCTATT CACATCCAGA AGCAGCCAA GACCGCCGAA ACTTGGTCTT	540
ATCTGAAATG AAAAATCAAG GCTACATCTC TGCTGAACAG TATGAGAAAG CAGTCAATAC	600
ACCAATTACT GATGGACTAC AAAGTCTCAA ATCAGCAAGT AATTACCTG CTTACATGGA	660
TAATTACCTC AAGGAAGTCA TCAATCAAGT TGAAGAAGAA ACAGGCTATA ACCTACTCAC	720
AACTGGGATG GATGTCTACA CAAATGTAGA CCAAGAAGCT CAAAAACATC TGTGGGATAT	780
TTACAATACA GACGAATACG TTGCCTATCC AGACGATGAA TTGCAAGTCG CTTCTACCAT	840
TGTTGATGTT TCTAACGGTA AAGTCATTGC CCAGCTAGGA GCACGCCATC AGTCAAGTAA	900
TGTTTCTTC GGAATTAAACC AAGCAGTAGA AACAAACCGC GACTGGGAT CAACTATGAA	960
ACCGATCACA GACTATGCTC CTGCCTTGGA GTACGGTGTC TACGATTCAA CTGCTACTAT	1020
CGTTCACGAT GAGCCCTATA ACTACCTGG GACAAATTACT CCTGTTATA ACTGGGATAG	1080
GGGCTACTTT GGCAACATCA CCTTGCAATA CGCCCTGCAA CAATCGCGAA ACGTCCCAGC	1140
CGTGGAAACT CTAAACAAGG TCGGACTCAA CCGCGCCAAG ACTTTCTAA ATGGTCTAGG	1200
AATCGACTAC CCAAGTATTG ACTACTCAA TGCCATTCA AGTAACACAA CCGAATCAGA	1260
CAAAAAATAT GGAGCAAGTA GTGAAAAGAT GGCTGCTGCT TACGCTGCCT TTGCAAATGG	1320
TGGAACCTAC TATAAACCAA TGTATATCCA TAAAGTCGTC TTTAGTGATG GGAGTGAAA	1380
AGAGTTCTCT AATGTCGGAA CTCGTGCCAT GAAGGAAACG ACAGCCTATA TGATGACCGA	1440
CATGATGAAA ACAGTCTTGA CTTATGGAAC TGGACGAAAT GCCTATCTTGCCTGGCTCCC	1500
TCAGGGCTGGT AAAACAGGAA CCTCTAACTA TACAGACGAG GAAATTGAAA ACCACATCAA	1560
GACCTCTCAA TTTGTAGCAC CTGATGAACT ATTTGCTGGC TATACCGCTA AATATTCAAT	1620
GGCTGTATGG ACAGGCTATT CTAACCGTCT GACACCACTT GTAGGCAATG GCCTTACGGT	1680
CGCTGCCAAA GTTTACCGCT CTATGATGAC CTACCTGTCT GAAGGAAAGCA ATCCAGAAGA	1740

TTGGAATATA CCAGAGGGGC TCTACAGAAA TGGAGAATTG GTATTTAAAA ATGGTGCTCG	1800
TTCTACGTGG AACTCACCTG CTCCACAACA ACCCCCATCA ACTGAAAGTT CAAGCTCATC	1860
ATCAGATAGT TCAACTTCAC AGTCTAGCTC ACCCACTCCA AGCACAAATA ATAGTACGAC	1920
TACCAATCCT AACAAATAATA CGCAACAATC AAATACAACC CCTGATCAAC AAAATCAGAA	1980
TCCTCAACCA GCACAAACCA	1999

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 666 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Ile Tyr Asp Asn Lys Asn Gln Leu Ile Ala Asp Leu Gly Ser Glu	
1 5 10 15	

Arg Arg Val Asn Ala Gln Ala Asn Asp Ile Pro Thr Asp Leu Val Lys	
20 25 30	

Ala Ile Val Ser Ile Glu Asp His Arg Phe Phe Asp His Arg Gly Ile	
35 40 45	

Asp Thr Ile Arg Ile Leu Gly Ala Phe Leu Arg Asn Leu Gln Ser Asn	
50 55 60	

Ser Leu Gln Gly Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Leu Thr	
65 70 75 80	

Tyr Phe Ser Thr Ser Asp Gln Thr Ile Ser Arg Lys Ala Gln	
85 90 95	

Glu Ala Trp Leu Ala Ile Gln Leu Glu Gln Lys Ala Thr Lys Gln Glu	
100 105 110	

Ile Leu Thr Tyr Tyr Ile Asn Lys Val Tyr Met Ser Asn Gly Asn Tyr	
115 120 125	

Gly Met Gln Thr Ala Ala Gln Asn Tyr Tyr Gly Lys Asp Leu Asn Asn	
130 135 140	

Leu Ser Leu Pro Gln Leu Ala Leu Leu Ala Gly Met Pro Gln Ala Pro	
145 150 155 160	

Asn Gln Tyr Asp Pro Tyr Ser His Pro Glu Ala Ala Gln Asp Arg Arg	
165 170 175	

Asn Leu Val Leu Ser Glu Met Lys Asn Gln Gly Tyr Ile Ser Ala Glu	
180 185 190	

Gln Tyr Glu Lys Ala Val Asn Thr Pro Ile Thr Asp Gly Leu Gln Ser	
195 200 205	

Leu Lys Ser Ala Ser Asn Tyr Pro Ala Tyr Met Asp Asn Tyr Leu Lys	
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210

215

220

Glu Val Ile Asn Gln Val Glu Glu Glu Thr Gly Tyr Asn Leu Leu Thr
 225 230 235 240

Thr Gly Met Asp Val Tyr Thr Asn Val Asp Gln Glu Ala Gln Lys His
 245 250 255

Leu Trp Asp Ile Tyr Asn Thr Asp Glu Tyr Val Ala Tyr Pro Asp Asp
 260 265 270

Glu Leu Gln Val Ala Ser Thr Ile Val Asp Val Ser Asn Gly Lys Val
 275 280 285

Ile Ala Gln Leu Gly Ala Arg His Gln Ser Ser Asn Val Ser Phe Gly
 290 295 300

Ile Asn Gln Ala Val Glu Thr Asn Arg Asp Trp Gly Ser Thr Met Lys
 305 310 315 320

Pro Ile Thr Asp Tyr Ala Pro Ala Leu Glu Tyr Gly Val Tyr Asp Ser
 325 330 335

Thr Ala Thr Ile Val His Asp Glu Pro Tyr Asn Tyr Pro Gly Thr Asn
 340 345 350

Thr Pro Val Tyr Asn Trp Asp Arg Gly Tyr Phe Gly Asn Ile Thr Leu
 355 360 365

Gln Tyr Ala Leu Gln Gln Ser Arg Asn Val Pro Ala Val Glu Thr Leu
 370 375 380

Asn Lys Val Gly Leu Asn Arg Ala Lys Thr Phe Leu Asn Gly Leu Gly
 385 390 395 400

Ile Asp Tyr Pro Ser Ile His Tyr Ser Asn Ala Ile Ser Ser Asn Thr
 405 410 415

Thr Glu Ser Asp Lys Lys Tyr Gly Ala Ser Ser Glu Lys Met Ala Ala
 420 425 430

Ala Tyr Ala Ala Phe Ala Asn Gly Gly Thr Tyr Tyr Lys Pro Met Tyr
 435 440 445

Ile His Lys Val Val Phe Ser Asp Gly Ser Glu Lys Glu Phe Ser Asn
 450 455 460

Val Gly Thr Arg Ala Met Lys Glu Thr Thr Ala Tyr Met Met Thr Asp
 465 470 475 480

Met Met Lys Thr Val Leu Thr Tyr Gly Thr Gly Arg Asn Ala Tyr Leu
 485 490 495

Ala Trp Leu Pro Gln Ala Gly Lys Thr Gly Thr Ser Asn Tyr Thr Asp
 500 505 510

Glu Glu Ile Glu Asn His Ile Lys Thr Ser Gln Phe Val Ala Pro Asp
 515 520 525

Glu Leu Phe Ala Gly Tyr Thr Arg Lys Tyr Ser Met Ala Val Trp Thr
 530 535 540

Gly Tyr Ser Asn Arg Leu Thr Pro Leu Val Gly Asn Gly Leu Thr Val

545	550	555	560
Ala Ala Lys Val Tyr Arg Ser Met Met Thr Tyr Leu Ser Glu Gly Ser			
565		570	575
Asn Pro Glu Asp Trp Asn Ile Pro Glu Gly Leu Tyr Arg Asn Gly Glu			
580	585		590
Phe Val Phe Lys Asn Gly Ala Arg Ser Thr Trp Asn Ser Pro Ala Pro			
595	600		605
Gln Gln Pro Pro Ser Thr Glu Ser Ser Ser Ser Ser Asp Ser Ser			
610	615		620
Thr Ser Gln Ser Ser Ser Thr Thr Pro Ser Thr Asn Asn Ser Thr Thr			
625	630	635	640
Thr Asn Pro Asn Asn Asn Thr Gln Gln Ser Asn Thr Thr Pro Asp Gln			
645		650	655
Gln Asn Gln Asn Pro Gln Pro Ala Gln Pro			
660	665		

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1714 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAATTACAAT ACGGACTATG AATTGACCTC TGGAGAAAAA TTACCTCTTC CTAAGAGAT	60
TTCAGGTTAC ACTTATATTG GATATATCAA AGAGGGAAAA ACGACTTCTG AGTCTGAAGT	120
AAGTAATCAA AAGAGTTCAAG TTGCCACTCC TACAAAACAA CAAAAGGTGG ATTATAATGT	180
TACACCGAAT TTTGTAGACC ATCCATCAAC AGTACAAGCT ATTCAAGAAC AAACACCTGT	240
TTCTTCAACT AAGCCGACAG AAGTTCAAGT AGTTGAAAAA CCTTTCTCTA CTGAATTAAT	300
CAATCCAAGA AAAGAAGAGA ACAATCTTC AGATTCTCAA GAACAATTAG CCGAACATAA	360
GAATCTAGAA ACGAAGAAAG AGGAGAAGAT TTCTCCAAAA GAAAAGACTG GGGTAAATAC	420
ATTAATCCA CAGGATGAAG TTTTATCAGG TCAATTGAAC AACCTGAAC TCTTATATCG	480
TGAGGAAACT ATGGAGACAA AAATAGATTT TCAAGAAGAA ATTCAAGAAA ATCCTGATTT	540
AGCTGAAGGA ACTGTAAGAG TAAAACAAGA AGGTAAATTG GGTAAGAAAG TTGAAATCGT	600
CAGAATATTC TCTGTAAACA AGGAAGAAGT TTCGCGAGAA ATTGTTCAA CTTCAACGAC	660
TGCGCCTAGT CCAAGAATAG TCGAAAAGG TACTAAAAAA ACTCAAGTTA TAAAGGAACA	720
ACCTGAGACT GGTGTAGAAC ATAAGGACGT ACAGTCTGGA GCTATTGTTG AACCCGCAAT	780
TCAGCCTGAG TTGCCCGAAG CTGTAGTAAG TGACAAAGGC GAACCAGAAG TTCAACCTAC	840

ATTACCCGAA	GCAGTTGTGA	CCGACAAAGG	TGAGACTGAG	GTCACCAG	AGTCGCCAGA	900
TACTGTGGTA	AGTGATAAAG	GTGAACCAGA	GCAGGTAGCA	CCGCTTCCAG	AATATAAGGG	960
TAATATTGAG	CAAGTAAAC	CTGAAAATC	GGTGAGAAG	ACCAAAGAAC	AAGGTCCAGA	1020
AAAAACTGAA	GAAGTTCCAG	TAAAACCAAC	AGAAGAAACA	CCAGTAAATC	CAAATGAAGG	1080
TACTACAGAA	GGAACCTCAA	TTCAAGAACG	AGAAAATCCA	GTCACCTG	CAGAAGAAC	1140
AACAACGAAT	TCAGAGAAAG	TATCACCAGA	TACATCTAGC	AAAAATACTG	GGGAAGTGTC	1200
CAGTAATCCT	AGTGATTGCA	CAACCTCAGT	TGGAGAATCA	AATAAACCGAG	AACATAATGA	1260
CTCTAAAAAT	GAAAATTGAG	AAAAAAACTGT	AGAAGAAGTT	CCAGTAAATC	CAAATGAAGG	1320
CACAGTAGAA	GGTACCTCAA	ATCAAGAAC	AGAAAAACCA	GTCACCTG	CAGAAGAAC	1380
ACAAACAAAC	TCTGGGAAAA	TAGCTAACGA	AAATACTGGA	GAAGTATCCA	ATAAACCTAG	1440
TGATTCAAAA	CCACCAGTTG	AAGAATCAAA	TCAACCAGAA	AAAAACGGAA	CTGCAACAAA	1500
ACCAGAAAAT	TCAGGTAATA	CAACATCAGA	GAATGGACAA	ACAGAACCGAG	AACCATCAA	1560
CGGAAATTCA	ACTGAGGATG	TTCAACCGA	ATCAAACACA	TCCAATTCAA	ATGGAAACGA	1620
AGAAATTAAA	CAAGAAAATG	AACTAGACCC	TGATAAAAAG	GTAGAAGAAC	CAGAGAAAAC	1680
ACTTGAATTA	AGAAATGTTT	CCGACCTAGA	GTAA			1714

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 571 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asn	Tyr	Asn	Thr	Asp	Tyr	Glu	Leu	Thr	Ser	Gly	Glu	Lys	Leu	Pro	Leu
1					5				10			15			
Pro	Lys	Glu	Ile	Ser	Gly	Tyr	Thr	Tyr	Ile	Gly	Tyr	Ile	Lys	Glu	Gly
			20				25				30				
Lys	Thr	Thr	Ser	Glu	Ser	Glu	Val	Ser	Asn	Gln	Lys	Ser	Ser	Val	Ala
			35				40				45				
Thr	Pro	Thr	Lys	Gln	Gln	Lys	Val	Asp	Tyr	Asn	Val	Thr	Pro	Asn	Phe
	50					55				60					
Val	Asp	His	Pro	Ser	Thr	Val	Gln	Ala	Ile	Gln	Glu	Gln	Thr	Pro	Val
65					70				75			80			
Ser	Ser	Thr	Lys	Pro	Thr	Glu	Val	Gln	Val	Val	Glu	Lys	Pro	Phe	Ser
			85				90					95			
Thr	Glu	Leu	Ile	Asn	Pro	Arg	Lys	Glu	Glu	Lys	Gln	Ser	Ser	Asp	Ser
			100				105					110			

Gln Glu Gln Leu Ala Glu His Lys Asn Leu Glu Thr Lys Lys Glu Glu
 115 120 125
 Lys Ile Ser Pro Lys Glu Lys Thr Gly Val Asn Thr Leu Asn Pro Gln
 130 135 140
 Asp Glu Val Leu Ser Gly Gln Leu Asn Lys Pro Glu Leu Leu Tyr Arg
 145 150 155 160
 Glu Glu Thr Met Glu Thr Lys Ile Asp Phe Gln Glu Glu Ile Gln Glu
 165 170 175
 Asn Pro Asp Leu Ala Glu Gly Thr Val Arg Val Lys Gln Glu Gly Lys
 180 185 190
 Leu Gly Lys Lys Val Glu Ile Val Arg Ile Phe Ser Val Asn Lys Glu
 195 200 205
 Glu Val Ser Arg Glu Ile Val Ser Thr Ser Thr Ala Pro Ser Pro
 210 215 220
 Arg Ile Val Glu Lys Gly Thr Lys Lys Thr Gln Val Ile Lys Glu Gln
 225 230 235 240
 Pro Glu Thr Gly Val Glu His Lys Asp Val Gln Ser Gly Ala Ile Val
 245 250 255
 Glu Pro Ala Ile Gln Pro Glu Leu Pro Glu Ala Val Val Ser Asp Lys
 260 265 270
 Gly Glu Pro Glu Val Gln Pro Thr Leu Pro Glu Ala Val Val Thr Asp
 275 280 285
 Lys Gly Glu Thr Glu Val Gln Pro Glu Ser Pro Asp Thr Val Val Ser
 290 295 300
 Asp Lys Gly Glu Pro Glu Gln Val Ala Pro Leu Pro Glu Tyr Lys Gly
 305 310 315 320
 Asn Ile Glu Gln Val Lys Pro Glu Thr Pro Val Glu Lys Thr Lys Glu
 325 330 335
 Gln Gly Pro Glu Lys Thr Glu Glu Val Pro Val Lys Pro Thr Glu Glu
 340 345 350
 Thr Pro Val Asn Pro Asn Glu Gly Thr Thr Glu Gly Thr Ser Ile Gln
 355 360 365
 Glu Ala Glu Asn Pro Val Gln Pro Ala Glu Glu Ser Thr Thr Asn Ser
 370 375 380
 Glu Lys Val Ser Pro Asp Thr Ser Ser Lys Asn Thr Gly Glu Val Ser
 385 390 395 400
 Ser Asn Pro Ser Asp Ser Thr Thr Ser Val Gly Glu Ser Asn Lys Pro
 405 410 415
 Glu His Asn Asp Ser Lys Asn Glu Asn Ser Glu Lys Thr Val Glu Glu
 420 425 430
 Val Pro Val Asn Pro Asn Glu Gly Thr Val Glu Gly Thr Ser Asn Gln
 435 440 445

Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn Ser
 450 455 460
 Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro Ser
 465 470 475 480
 Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn Gly
 485 490 495
 Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn Gly
 500 505 510
 Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val Ser
 515 520 525
 Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys Gln
 530 535 540
 Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys Thr
 545 550 555 560
 Leu Glu Leu Arg Asn Val Ser Asp Leu Glu Leu
 565 570

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 748 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGAGAATCAA GCTACACCCA AAGAGACTAG CGCTAAAAG ACAATCGTCC TTGCTACAGC	60
TGGCGACGTG CCACCATTG ACTACGAAGA CAAGGGCAAT CTGACAGGCT TTGATATCGA	120
AGTTTTAAAG GCAGTAGATG AAAAACTCAG CGACTACGAG ATTCAATTCC AAAGAACCGC	180
CTGGGAGAGC ATCTTCCCAG GACTTGATTC TGGTCACTAT CAGGCTGCAG CCAATAACTT	240
GAGTTACACA AAAGAGCGTG CTGAAAAATA CCTTTACTCG CTTCCAATTT CCAACAATCC	300
CCTCGTCCTT GTCAGCAACA AGAAAAATCC TTTGACTTCT CTTGACCAGA TCGCTGGTAA	360
AACAACACAA GAGGATACCG GAACTTCTAA CGCTCAATTG ATCAATAACT GGAATCAGAA	420
ACACACTGAT AATCCCGCTA CAATTAATTG TTCTGGTGAG GATATTGGTA AACGAATCCT	480
AGACCTTGCT AACGGAGAGT TTGATTTCT AGTTTTGAC AAGGTATCCG TTCAAAAGAT	540
TATCAAGGAC CGTGGTTAG ACCTCTCAGT CGTTGATTG CCTTCTGCAG ATAGCCCCAG	600
CAATTATATC ATTTTCTCAA GCGACCAAAA AGAGTTAAA GAGCAATTG ATAAAGCGCT	660
CAAAGAACTC TATCAAGACG GAACCCCTGA AAAACTCAGC AATACCTATC TAGGTGGTTC	720
TTACCTCCCA GATCAATCTC AGTTACAA	748

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu	Asn	Gln	Ala	Thr	Pro	Lys	Glu	Thr	Ser	Ala	Gln	Lys	Thr	Ile	Val
1							5			10				15	

Leu	Ala	Thr	Ala	Gly	Asp	Val	Pro	Pro	Phe	Asp	Tyr	Glu	Asp	Lys	Gly
							20		25				30		

Asn	Leu	Thr	Gly	Phe	Asp	Ile	Glu	Val	Leu	Lys	Ala	Val	Asp	Glu	Lys
						35		40			45				

Leu	Ser	Asp	Tyr	Glu	Ile	Gln	Phe	Gln	Arg	Thr	Ala	Trp	Glu	Ser	Ile
					50		55			60					

Phe	Pro	Gly	Leu	Asp	Ser	Gly	His	Tyr	Gln	Ala	Ala	Ala	Asn	Asn	Leu
					65		70		75			80			

Ser	Tyr	Thr	Lys	Glu	Arg	Ala	Glu	Lys	Tyr	Leu	Tyr	Ser	Leu	Pro	Ile
					85			90			95				

Ser	Asn	Asn	Pro	Leu	Val	Leu	Val	Ser	Asn	Lys	Lys	Asn	Pro	Leu	Thr
					100			105			110				

Ser	Leu	Asp	Gln	Ile	Ala	Gly	Lys	Thr	Thr	Gln	Glu	Asp	Thr	Gly	Thr
					115		120			125					

Ser	Asn	Ala	Gln	Phe	Ile	Asn	Asn	Trp	Asn	Gln	Lys	His	Thr	Asp	Asn
					130		135			140					

Pro	Ala	Thr	Ile	Asn	Phe	Ser	Gly	Glu	Asp	Ile	Gly	Lys	Arg	Ile	Leu
					145		150		155		160				

Asp	Leu	Ala	Asn	Gly	Glu	Phe	Asp	Phe	Leu	Val	Phe	Asp	Lys	Val	Ser
					165			170			175				

Val	Gln	Lys	Ile	Ile	Lys	Asp	Arg	Gly	Leu	Asp	Leu	Ser	Val	Val	Asp
					180			185			190				

Leu	Pro	Ser	Ala	Asp	Ser	Pro	Ser	Asn	Tyr	Ile	Ile	Phe	Ser	Ser	Asp
					195			200			205				

Gln	Lys	Glu	Phe	Lys	Glu	Gln	Phe	Asp	Lys	Ala	Leu	Lys	Glu	Leu	Tyr
					210		215			220					

Gln	Asp	Gly	Thr	Leu	Glu	Lys	Leu	Ser	Asn	Thr	Tyr	Leu	Gly	Gly	Ser
					225		230			235			240		

Tyr	Leu	Pro	Asp	Gln	Ser	Gln	Leu	Gln						
					245									

(2) INFORMATION FOR SEQ ID NO: 7:

DECODED SEQUENCE

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 985 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGGTAACCGC TCTTCTCGTA ACGCAGCTTC ATCTTCTGAT GTGAAGACAA AAGCAGCAAT	60
CGTCACTGAT ACTGGTGGTG TTGATGACAA ATCATTCAAC CAATCAGCTT GGGAGGTTT	120
GCAGGCTTGG GCTAAAGAAC ACAATCTTC AAAAGATAAC GGTTTCACTT ACTTCCAATC	180
AACAAGTGAA GCTGACTACG CTAACAAC TT GCAACAAGCG GCTGGAAGTT ACAACCTAAT	240
CTTCGGTGTGTT GGTTTGCCC TTAATAATGC AGTTAAAGAT GCAGCAAAG AACACACTGA	300
CTTGAACATAT GTCTTGATTG ATGATGTGAT TAAAGACCA AAGAATGTTG CGAGCGTAAC	360
TTTCGCTGAT AATGAGTCAG GTTACCTTGC AGGTGTTGGCT GCAGCAAAAA CAACTAAGAC	420
AAAACAAGTT GGTTTTGTAG GTGGTATCGA ATCTGAAGTT ATCTCTCGTT TTGAAGCAGG	480
ATTCAAGGCT GGTGTTGCGT CAGTAGACCC ATCTATCAA GTCCAAGTTG ACTACGCTGG	540
TTCATTTGGT GATGCGGCTA AAGGTAAAAC AATTGCAGCC GCACAATACG CAGCCGGTGC	600
AGATATTGTT TACCAAGTAG CTGGTGGTAC AGGTGCAGGT GTCTTGCAG AGGCAAAATC	660
TCTCAACGAA AGCCGTCTG AAAATGAAAA AGTTGGTT ATCGGTGTTG ATCGTGACCA	720
AGAAGCAGAA GGTAAATACA CTTCTAAAGA TGGCAAAGAA TCAAACTTTG TTCTTGTATC	780
TACTTTGAAA CAAGTTGGTA CAACTGTAAA AGATATTCT AACAAAGGCAG AAAGAGGAGA	840
ATTCCCTGGC GGTCAAGTGA TCGTTTACTC ATTGAAGGAT AAAGGGTTG ACTTGGCAGT	900
AACAAACCTT TCAGAAGAAG GTAAAAAAGC TGTGAAAGAT GCAAAAGCTA AAATCCTTGA	960
TGGAAGCGTA AAAGTTCTG AAAAA	985

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser Ser Ser Asp Val Lys Thr	
1 5 10 15	

Lys Ala Ala Ile Val Thr Asp Thr Gly Gly Val Asp Asp Lys Ser Phe	
20 25 30	

Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala Trp Gly Lys Glu His Asn	
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35	40	45
Leu Ser Lys Asp Asn Gly Phe Thr Tyr Phe Gln Ser Thr Ser Glu Ala		
50	55	60
Asp Tyr Ala Asn Asn Leu Gln Gln Ala Ala Gly Ser Tyr Asn Leu Ile		
65	70	75
Phe Gly Val Gly Phe Ala Leu Asn Asn Ala Val Lys Asp Ala Ala Lys		
85	90	95
Glu His Thr Asp Leu Asn Tyr Val Leu Ile Asp Asp Val Ile Lys Asp		
100	105	110
Gln Lys Asn Val Ala Ser Val Thr Phe Ala Asp Asn Glu Ser Gly Tyr		
115	120	125
Leu Ala Gly Val Ala Ala Ala Lys Thr Thr Lys Thr Lys Gln Val Gly		
130	135	140
Phe Val Gly Gly Ile Glu Ser Glu Val Ile Ser Arg Phe Glu Ala Gly		
145	150	155
160		
Phe Lys Ala Gly Val Ala Ser Val Asp Pro Ser Ile Lys Val Gln Val		
165	170	175
Asp Tyr Ala Gly Ser Phe Gly Asp Ala Ala Lys Gly Lys Thr Ile Ala		
180	185	190
Ala Ala Gln Tyr Ala Ala Gly Ala Asp Ile Val Tyr Gln Val Ala Gly		
195	200	205
Gly Thr Gly Ala Gly Val Phe Ala Glu Ala Lys Ser Leu Asn Glu Ser		
210	215	220
Arg Pro Glu Asn Glu Lys Val Trp Val Ile Gly Val Asp Arg Asp Gln		
225	230	235
240		
Glu Ala Glu Gly Lys Tyr Thr Ser Lys Asp Gly Lys Glu Ser Asn Phe		
245	250	255
Val Leu Val Ser Thr Leu Lys Gln Val Gly Thr Thr Val Lys Asp Ile		
260	265	270
Ser Asn Lys Ala Glu Arg Gly Glu Phe Pro Gly Gly Gln Val Ile Val		
275	280	285
Tyr Ser Leu Lys Asp Lys Gly Val Asp Leu Ala Val Thr Asn Leu Ser		
290	295	300
Glu Glu Gly Lys Lys Ala Val Glu Asp Ala Lys Ala Lys Ile Leu Asp		
305	310	315
320		
Gly Ser Val Lys Val Pro Glu Lys		
325		

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGCTGATT CAGGTGACAA ACCTGTTATC 60
 AAAATGTACC AAATCGGTGA CAAACCAGAC AACTTGGATG AATTGTTAGC AAATGCCAAC 120
 AAAATCATTG AAGAAAAAGT TGGTGCCTAA TTGGATATCC AATACCTTGG CTGGGGTGAC 180
 TATGGTAAGA AAATGTCAGT TATCACATCA TCTGGTAAA ACTATGATAT TGCCTTGCA 240
 GATAACTATA TTGTAATGC TCAAAAAGGT GCTTACGCTG ACTTGACAGA ATTGTACAAA 300
 AAAGAAGGTA AAGACCTTTA CAAAGCAGTT GACCCAGCTT ACATCAAGGG TAATACTGTA 360
 AATGGTAAGA TTTACGCTGT TCCAGTTGCA GCCAACGTTG CATCATCTCA AAACCTTGCC 420
 TTCAACGGAA CTCTCCTTGC TAAATATGGT ATCGATATTT CAGGTGTTAC TTCTTACGAA 480
 ACTCTTGAGC CAGTCTTGAA ACAAAATCAA GAAAAAGCTC CAGACGTAGT ACCATTTGCT 540
 ATTGGTAAAG TTTTCATCCC ATCTGATAAT TTTGACTACC CAGTAGCAA CGGTCTTCCA 600
 TTCGTTATCG ACCTTGAAGG CGATACTACT AAAGTTGTAA ACCGTTACGA AGTGCCTCGT 660
 TTCAAAGAAC ACTTGAAGAC TCTTCACAAA TTCTATGAAG CTGGCTACAT TCCAAAAGAC 720
 GTCGCAACAA GCGATACTTC CTTTGACCTT CAACAAGATA CTTGGTTCGT TCGTGAAGAA 780
 ACAGTAGGAC CAGCTGACTA CGGTAACAGC TTGCTTCAC GTGTTGCCAA CAAAGATATC 840
 CAAATCAAAC CAATTACTAA CTTCATCAAG NAAAACCAA CAACACAAGT TGCTAACTTT 900
 GTCATCTCAA ACAACTCTAA GAACAAAGAA AAATCAATGG AAATCTTGAA CCTCTTGAAT 960
 ACGAACCCAG AACTCTTGAA CGGTCTTGT TACGGTCCAG AAGGCAAGAA CTGGAAAAAA 1020
 ATTGAAGGTA AAGAAAACCG TGTTCGCGTT CTTGATGGCT ACAAAAGGAAA CACTCACATG 1080
 GGTGGATGGA ACACTGGTAA CAACTGGATC CTTTACATCA ACGAAAACGT TACAGACCAA 1140
 CAAATCGAAA ATTCTAAGAA AGAATTGGCA GAAGCTAAAG AATCTCCAGC GCTTGGATTT 1200
 ATCTTCATAA CTGACAATGT GAAATCTGAA ATCTCAGCTA TTGCTAACAC AATGCAACAA 1260
 TTTGATACAG CTATCAACAC TGGTACTGTA GACCCAGATA AAGCGATTCC AGAATTGATG 1320
 GAAAAATTGA AATCTGAAGG TGCCTACGAA AAAGTATTGA ACGAAATGCA AAAACAATAC 1380
 GATGAATTCT TGAAAAACAA AAAA 1404

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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